

SEQUENCE LISTING

<110> Farnham, Peggy J.
Graveel, Carrie R.
Harkins-Perry, Sarah R.

<120> Liver Tumor marker Sequences

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<150> 60/396, 626
<151> 2002-07-17

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<170> PatentIn Ver. 2.1

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sequence reads aaccattaaaaaaaaaaaaaaaaaaagt

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<223> From this position forward, second variant 3' UTR
sequence reads
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Val Pro Ile Arg Val Met Ile Asp Leu Cys Asn Ser Thr Gln Gly Ile
10 15 20 25

tgc ctc aca gga cca ccc ggc cca cca gga cct cca gga gcc ggc ggg 147
Cys Leu Thr Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ala Gly Gly
30 35 40

tta cca ggc cac aat gga tca gat gga cag cct ggt ctc cag ggc cca 195
Leu Pro Gly His Asn Gly Ser Asp Gly Gln Pro Gly Leu Gln Gly Pro

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gaa ctg ggt cta cct gga aat gag ggc cca cca ggg cag aaa ggt gac Glu Leu Gly Leu Pro Gly Asn Glu Gly Pro Pro Gly Gln Lys Gly Asp 90 95 100 105			339
aag gga gac aaa gga gac gtg tcc aat gac gtg ctt ttg aca ggt gcc Lys Gly Asp Lys Gly Asp Val Ser Asn Asp Val Leu Leu Thr Gly Ala 110 115 120			387
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acc ttg gtg gga aga gct gat gag aaa gca aat gaa cgc cat tca cca Thr Leu Val Gly Arg Ala Asp Glu Lys Ala Asn Glu Arg His Ser Pro 170 175 180 185			579
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aag gag ttc aaa gac ctg ccg gcg ctc ctc aat agc agc ttc acc ctc Lys Glu Phe Lys Asp Leu Pro Ala Leu Leu Asn Ser Ser Phe Thr Leu 235 240 245			771
ctc cac ctc cca cat tat ttc cac ggc tgt ggg cac gct gtt tac aac Leu His Leu Pro His Tyr Phe His Gly Cys Gly His Ala Val Tyr Asn 250 255 260 265			819
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 Tyr Phe Asp Arg Lys Tyr Leu Phe Ala Asn Ser Lys Thr Tyr Phe Asn
 300 305 310

 ata gca gtg gat gag aag ggc atc tgg att atc tac gct tca agt gtg 1011
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 315 320 325

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35 40 45

Asp Gly Gln Pro Gly Leu Gln Gly Pro Lys Gly Glu Lys Gly Ala Ile
50 55 60

Gly Lys Arg Gly Lys Met Gly Leu Pro Gly Ala Thr Gly Asn Pro Gly
65 70 75 80

Glu Lys Gly Glu Lys Gly Asp Ala Gly Glu Leu Gly Leu Pro Gly Asn
85 90 95

Glu Gly Pro Pro Gly Gln Lys Gly Asp Lys Gly Asp Lys Gly Asp Val
100 105 110

Ser Asn Asp Val Leu Leu Thr Gly Ala Lys Gly Asp Gln Gly Pro Pro
115 120 125

Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Ser Arg Arg
130 135 140

Ser Lys Gly Pro Arg Pro Pro Asn Val Phe Asn Ser Gln Cys Pro Gly
145 150 155 160

Glu Thr Cys Val Ile Pro Asn Asp Asp Thr Leu Val Gly Arg Ala Asp
165 170 175

Glu Lys Ala Asn Glu Arg His Ser Pro Gln Thr Glu Ser Met Ile Thr
180 185 190

Ser Ile Gly Asn Pro Ala Gln Val Leu Lys Val Arg Glu Thr Phe Gly
195 200 205

Thr Trp Met Arg Glu Ser Ala Asn Lys Ser Asp Asp Arg Ile Trp Val
210 215 220

Thr Glu His Phe Ser Gly Ile Met Val Lys Glu Phe Lys Asp Leu Pro
225 230 235 240

Ala Leu Leu Asn Ser Ser Phe Thr Leu Leu His Leu Pro His Tyr Phe
245 250 255

His Gly Cys Gly His Ala Val Tyr Asn Asn Ser Leu Tyr Tyr His Lys
260 265 270

Gly Gly Ser Asn Thr Ile Val Arg Phe Glu Phe Gly Lys Glu Thr Pro
275 280 285

Gln Thr Leu Lys Leu Glu Asn Ala Leu Tyr Phe Asp Arg Lys Tyr Leu
290 295 300

Phe Ala Asn Ser Lys Thr Tyr Phe Asn Ile Ala Val Asp Glu Lys Gly
305 310 315 320

Ile Trp Ile Ile Tyr Ala Ser Ser Val Asp Gly Ser Ser Ile Leu Val
325 330 335

Ala Gln Leu Asp Gly Arg Thr Phe Ser Val Thr Gln His Ile Asn Thr
340 345 350

Thr Tyr Pro Lys Ser Lys Ala Gly Asn Ala Phe Ile Ala Arg Gly Ile
355 360 365

Leu Tyr Val Thr Asp Thr Lys Asp Thr Arg Val Thr Phe Ala Phe Asp
370 375 380

Leu Leu Gly Gly Lys Gln Ile Asn Ala Asn Phe Asp Phe Arg Met Ser
385 390 395 400

Gln Ser Val Leu Ala Met Leu Ser Tyr Asn Met Arg Asp Gln His Leu
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Asp Leu Cys Asn Ser Thr Lys Gly Ile Cys Leu Thr Gly Pro Pro Gly
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gcc ggc ggg ttg cca gga cac aac gga ttg gat gga cag cct ggt cct 144
Ala Gly Gly Leu Pro Gly His Asn Gly Leu Asp Gly Gln Pro Gly Pro
35 40 45

cag ggc cca aaa gga gaa aaa gga gca aat gga aaa aga gga aaa atg 192
Gln Gly Pro Lys Gly Glu Lys Gly Ala Asn Gly Lys Arg Gly Lys Met
50 55 60

ggg ata cct gga gct gca gga aat cca ggg gaa agg gga gaa aag gga 240
Gly Ile Pro Gly Ala Ala Gly Asn Pro Gly Glu Arg Gly Glu Lys Gly
65 70 75 80

gac cat ggt gaa ctg ggc ctg cag gga aat gag ggc cca cca ggg cag 288
Asp His Gly Glu Leu Gly Leu Gln Gly Asn Glu Gly Pro Pro Gly Gln
85 90 95

aag gga gaa aag ggt gac aaa gga gat gtg tcc aac gac gtg ctc ctg 336
Lys Gly Glu Lys Gly Asp Lys Gly Asp Val Ser Asn Asp Val Leu Leu
100 105 110

ggt gcc aaa ggt gac caa ggc cca ccc ggt cca cct ggg ccc cca ggc 384
Gly Ala Lys Gly Asp Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
115 120 125

cct cca ggt cct cca ggg ccc cct gga agc aga aga gcc aaa ggc cct 432
Pro Pro Gly Pro Pro Gly Pro Pro Gly Ser Arg Arg Ala Lys Gly Pro
130 135 140

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Arg Gln Pro Ser Met Phe Asn Gly Gln Cys Pro Gly Glu Thr Cys Ala
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35 40 45

Gln Gly Pro Lys Gly Glu Lys Gly Ala Asn Gly Lys Arg Gly Lys Met
50 55 60

Gly Ile Pro Gly Ala Ala Gly Asn Pro Gly Glu Arg Gly Glu Lys Gly
65 70 75 80

Asp His Gly Glu Leu Gly Leu Gln Gly Asn Glu Gly Pro Pro Gly Gln
85 90 95

Lys Gly Glu Lys Gly Asp Lys Gly Asp Val Ser Asn Asp Val Leu Leu
100 105 110

Gly Ala Lys Gly Asp Gln Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly
115 120 125

Pro Pro Gly Pro Pro Gly Pro Pro Gly Ser Arg Arg Ala Lys Gly Pro
130 135 140

Arg Gln Pro Ser Met Phe Asn Gly Gln Cys Pro Gly Glu Thr Cys Ala
145 150 155 160

Ile Pro Asn Asp Asp Thr Leu Val Gly Lys Ala Asp Glu Lys Ala Lys
165 170 175

Ser Met Ile Thr Ser Ile Gly Asn Pro Val Gln Val Leu Lys Val Thr
180 185 190

Glu Thr Phe Gly Thr Trp Ile Arg Glu Ser Ala Asn Lys Ser Asp Asp
195 200 205

Arg Ile Trp Val Thr Glu His Phe Ser Gly Pro Pro Ser Ile Leu Phe
210 215 220

Pro Trp Leu Trp Ala Arg Cys Leu Gln Gln Leu Ser Leu Leu Pro Gln
225 230 235 240

Arg Gly Phe Glu Phe Gly Gln Glu Thr Ser Gln Thr Leu Lys Leu Glu
245 250 255

Asn Ala Leu Tyr Phe Asp Arg Lys Tyr Leu Phe Ala Asn Ser Lys Thr
260 265 270

Tyr Phe Asn Leu Ala Val Asp Glu Lys Gly Leu Trp Ile Ile Tyr Ala
275 280 285

Ser Ser Val Asp Gly Ser Ser Ile Leu Val Ala Gln Leu Asp Glu Arg
290 295 300

Thr Phe Ser Val Val Gln His Val Asn Thr Thr Tyr Pro Lys Ser Lys
305 310 315 320

Ala Gly Asn Ala Phe Ile Ala Arg Gly Ile Leu Tyr Val Thr Asp Thr
325 330 335

Lys Asp Met Arg Val Thr Phe Ala Phe Asp Leu Leu Gly Gly Lys Gln
340 345 350

Ile Asn Ala Asn Phe Asp Leu Arg Thr Ser Gln Ser Val Leu Ala Met
355 360 365

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His Leu Met Leu Tyr Pro Val Gln Phe Leu Ser Thr Thr Leu Asn Gln
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<210> 6
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<220>
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